

**EXHIBIT A**

**CLUSTAL W (1.7) Multiple Sequence Alignments**

Sequence format is Pearson  
Sequence 1: PF0148\_3CPA\_SEQIDNO1 289 aa  
Sequence 2: gi4583152 282 aa  
Start of Pairwise alignments  
Aligning...  
Sequences (1:2) Aligned. Score: 99  
Start of Multiple Alignment  
There are 1 groups  
Aligning...  
Group 1: Sequences: 2 Score:3912  
Alignment Score 1827  
CLUSTAL-Alignment file created [baaTpakK.aln]  
CLUSTAL W (1.7) multiple sequence alignment

PF0148_3CPA_SEQIDNO1 gi4583152	MSGFSTEERAAPFSLEYRVFLKNEKGQYISPFHDIPYADKDVFMVVEVPRWSNAKMEI ----STEERAAAFSLEYRVFLKNEKGQYISPFHDIPYADKDVFMVVEVPRWSNAKMEI *****
PF0148_3CPA_SEQIDNO1 gi4583152	ATKDPLNPIKQDVKKGKLRYVANLFPYKGYIWNYGAI PQTWEDPGHNDKHTGCCGDNDPI ATKDPLNPIKQDVKKGKLRYVANLFPYKGYIWNYGAI PQTWEDPGHNDKHTGCCGDNDPI *****
PF0148_3CPA_SEQIDNO1 gi4583152	DVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRLKP DVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRLKP *****
PF0148_3CPA_SEQIDNO1 gi4583152	GYLEATVDWFRRYKVPDGKPENEFAFNAEFDKDFAIIDIICKSTHDHWKALVTKKTNGKGI GYLEATVDWFRRYKVPDGKPENEFAFNAEFDKDFAIIDIICKSTHDHWKALVTKKTNGKGI *****
PF0148_3CPA_SEQIDNO1 gi4583152	SCMNTTLSESPFKCDPDAARAIVDALPPP CESACTVPTDVKWFHHQKN SCMNTTLSESPFKCDPDAARAIVDALPPP CESACTVPTDVKWFHH--- *****

The figure shows the NCBI Nucleotide search interface. At the top, there's a logo for NCBI and a sequence alignment of two DNA strands. The left strand has mutations marked with black hexagons. Below the alignment are search filters: 'Search' (with dropdown 'Nucleotide'), 'for' (with checked checkbox), 'Limits', 'Preview/Index', 'History', 'Clipboard', 'Display' (set to 'default'), 'Show' (set to '1'), 'Send to' (with dropdown 'File'), and buttons for 'Go' and 'Clear'. A large 'Nucleotide' button is on the right.

□ 1: AF108211. *Homo sapiens* cyto...[gi:4583152]

## Links

LOCUS AF108211 846 bp mRNA linear PRI 14-APR-1999  
 DEFINITION Homo sapiens cytosolic inorganic pyrophosphatase mRNA, partial cds.  
 ACCESSION AF108211  
 VERSION AF108211.1 GI:4583152  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 846)  
 REFERENCE Rumsfeld,J., Ziegelbauer,K. and Spaltmann,F.  
 AUTHORS  
 TITLE Cloning, expression, affinity purification and characterization of  
 polyhistidine-tagged cytosolic *Saccharomyces cerevisiae* and human  
 inorganic pyrophosphatases for differential screening of compounds  
 for antifungal activity  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 846)  
 AUTHORS Rumsfeld,J., Ziegelbauer,K. and Spaltmann,F.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-NOV-1998) Research Antiinfectives 1, Bayer AG, P.O.  
 Box 10179, Wuppertal 42096, Germany  
 FEATURES Location/Qualifiers  
 source 1..846  
 /organism="Homo sapiens"  
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 /cell\_line="BjAB"  
 /cell\_type="B-cell"  
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 NDKHTGCCGNDPVIDVCEIGSKVCARGEII  
 GVKVLGILAMIDEGETDWKVIAINVDF  
 DAANYNDINDVKRLKPGYLEATVDWFRRYKVPDGKPENEFAFNAEF  
 KDKDFAIDI  
 IKS  
 THDHWKALVTKKTNGKGISCMNTTLS  
 ESPFKCDPDAARAIVDALPPP  
 CESACTVPTDV  
 DKWFHH"  
 BASE COUNT 270 a 155 c 201 g 220 t  
 ORIGIN  
 1 agcaccgagg agcgccggc ggccttctcc ctggagtacc gagtcttcct caaaaatgag  
 61 aaaggacaat atatatctcc atttcatgat attccaattt atccagataa ggatgtgttt  
 121 cacatggtag ttgaagtacc acgctggct aatgcaaaaaa tggagattgc tacaaaggac  
 181 cctttaaacc ctatcaaaca agatgtaaaa aaaggaaaaac ttgcgtatgt tgcaatttg

241 ttcccgata aaggatatac ctggaaactat ggtgccatcc ctcagacttg ggaagaccca  
301 gggcacaatg ataaacatac tggctgttgt ggtgacaatg acccaattga tgtgtgtgaa  
361 atttggaaagca aggtatgtgc aagaggtgaa ataattggcg tgaaagttct aggcatttt  
421 gctatgattt acgaaggggaa aaccgactgg aaagtcatgg ccattaatgt ggatgatcct  
481 gatgcagcca attataatga tatcaatgtat gtcaaaccggc tgaaacctgg ctacttagaa  
541 gctactgtgg actggtttag aaggtataag gttcctgtatg gaaaaccaga aatgagttt  
601 gcgttaatg cagaatttaa agataaggac tttgccattt atattattaa aagcactcat  
661 gaccatttggaa aagcatttagt gactaagaaa acgaatggaa aaggaatcag ttgcatgaat  
721 acaaactttgt ctgagagccc cttcaagtgt gatcctgtatg ctgccagagc cattgtggat  
781 gcttaccac caccctgtga atctgcgtgc acagtaccaa cagacgtgga taagtggttc  
841 catcac

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